



SEQUENCE LISTING

<110> Iezu, Jun-Ichi
Oku, Asuka

Dollie
Az

<120> TRANSPORTER GENES

<130> 06501-057001

<140> 09/521,195

<141> 2000-03-07

<150> JP 10/156660

<151> 1998-05-20

<150> JP 9/260972

<151> 1997-09-08

<150> PCT/JP98/04009

<151> 1998-09-07

<160> 32

<210> 1

<211> 551

<212> PRT

<213> Homo sapiens

<400> 1

Met	Arg	Asp	Tyr	Asp	Glu	Val	Ile	Ala	Phe	Leu	Gly	Glu	Trp	Gly	Pro
1									5	10			15		
Phe	Gln	Arg	Leu	Ile	Phe	Phe	Leu	Leu	Ser	Ala	Ser	Ile	Ile	Pro	Asn
									20	25			30		
Gly	Phe	Asn	Gly	Met	Ser	Val	Val	Phe	Leu	Ala	Gly	Thr	Pro	Glu	His
									35	40		45			
Arg	Cys	Arg	Val	Pro	Asp	Ala	Ala	Asn	Leu	Ser	Ser	Ala	Trp	Arg	Asn
									50	55		60			
Asn	Ser	Val	Pro	Leu	Arg	Leu	Arg	Asp	Gly	Arg	Glu	Val	Pro	His	Ser
									65	70		75		80	
Cys	Ser	Arg	Tyr	Arg	Leu	Ala	Thr	Ile	Ala	Asn	Phe	Ser	Ala	Leu	Gly
									85	90		95			
Leu	Glu	Pro	Gly	Arg	Asp	Val	Asp	Leu	Gly	Gln	Leu	Glu	Gln	Glu	Ser
									100	105		110			
Cys	Leu	Asp	Gly	Trp	Glu	Phe	Ser	Gln	Asp	Val	Tyr	Leu	Ser	Thr	Val
									115	120		125			
Val	Thr	Glu	Trp	Asn	Leu	Val	Cys	Glu	Asp	Asn	Trp	Lys	Val	Pro	Leu
									130	135		140			
Thr	Thr	Ser	Leu	Phe	Phe	Val	Gly	Val	Leu	Leu	Gly	Ser	Phe	Val	Ser
									145	150		155		160	
Gly	Gln	Leu	Ser	Asp	Arg	Phe	Gly	Arg	Lys	Asn	Val	Leu	Phe	Ala	Thr
									165	170		175			
Met	Ala	Val	Gln	Thr	Gly	Phe	Ser	Phe	Leu	Gln	Ile	Phe	Ser	Ile	Ser
									180	185		190			
Trp	Glu	Met	Phe	Thr	Val	Leu	Phe	Val	Ile	Val	Gly	Met	Gly	Gln	Ile
									195	200		205			
Ser	Asn	Tyr	Val	Val	Ala	Phe	Ile	Leu	Gly	Thr	Glu	Ile	Leu	Gly	Lys
									210	215		220			

Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala
 225 230 235 240
 Val Gly Tyr Met Leu Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
 245 250 255
 Arg Met Leu Leu Leu Ala Leu Thr Val Pro Gly Val Leu Cys Val Pro
 260 265 270
 Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg
 275 280 285
 Arg Phe Arg Glu Ala Glu Asp Ile Ile Gln Lys Ala Ala Lys Met Asn
 290 295 300
 Asn Thr Ala Val Pro Ala Val Ile Phe Asp Ser Val Glu Glu Leu Asn
 305 310 315 320
 Pro Leu Lys Gln Gln Lys Ala Phe Ile Leu Asp Leu Phe Arg Thr Arg
 325 330 335
A1
 Asn Ile Ala Ile Met Thr Ile Met Ser Leu Leu Leu Trp Met Leu Thr
 340 345 350
 Ser Val Gly Tyr Phe Ala Leu Ser Leu Asp Ala Pro Asn Leu His Gly
 355 360 365
 Asp Ala Tyr Leu Asn Cys Phe Leu Ser Ala Leu Ile Glu Ile Pro Ala
 370 375 380
 Tyr Ile Thr Ala Trp Leu Leu Leu Arg Thr Leu Pro Arg Arg Tyr Ile
 385 390 395 400
 Ile Ala Ala Val Leu Phe Trp Gly Gly Val Leu Leu Phe Ile Gln
 405 410 415
 Leu Val Pro Val Asp Tyr Tyr Phe Leu Ser Ile Gly Leu Val Met Leu
 420 425 430
 Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val Phe Thr
 435 440 445
 Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly Val Thr
 450 455 460
 Ser Thr Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe Val Tyr
 465 470 475 480
 Leu Gly Ala Tyr Asn Arg Met Leu Pro Tyr Ile Val Met Gly Ser Leu
 485 490 495
 Thr Val Leu Ile Gly Ile Phe Thr Leu Phe Phe Pro Glu Ser Leu Gly
 500 505 510
 Met Thr Leu Pro Glu Thr Leu Glu Gln Met Gln Lys Val Lys Trp Phe
 515 520 525
 Arg Ser Gly Lys Lys Thr Arg Asp Ser Met Glu Thr Glu Glu Asn Pro
 530 535 540
 Lys Val Leu Ile Thr Ala Phe
 545 550

<210> 2
 <211> 2135
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (147)..(1799)

<400> 2
 cccggcttc gcgcccaat ttctaacagc ctgcctgtcc cccggaaacg ttctaacatc 60
 cttggggagc gccccagcta caagacactg tcctgagaac gctgtcatca cccgtatgg 120

caagtttcgg agcggcagtg ggaagc atg cgg gac tac gac gag gtg atc gcc 173
 Met Arg Asp Tyr Asp Glu Val Ile Ala
 1 5

ttc ctg ggc gag tgg ggg ccc ttc cag cgc ctc atc ttc ttc ctg ctc 221
 Phe Leu Gly Glu Trp Gly Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu
 10 15 20 25

agc gcc agc atc atc ccc aat ggc ttc aat ggt atg tca gtc gtg ttc 269
 Ser Ala Ser Ile Ile Pro Asn Gly Phe Asn Gly Met Ser Val Val Phe
 30 35 40

ctg gcg ggg acc ccg gag cac cgc tgt cga gtg ccg gac gcc gcg aac 317
 Leu Ala Gly Thr Pro Glu His Arg Cys Arg Val Pro Asp Ala Ala Asn
 45 50 55

A1
 ctg agc agc gcc tgg cgc aac aac agt gtc ccg ctg cgg ctg cgg gac 365
 Leu Ser Ser Ala Trp Arg Asn Asn Ser Val Pro Leu Arg Leu Arg Asp
 60 65 70

ggc cgc gag gtg ccc cac agc tgc agc cgc tac ccg ctc gcc acc atc 413
 Gly Arg Glu Val Pro His Ser Cys Ser Arg Tyr Arg Leu Ala Thr Ile
 75 80 85

gcc aac ttc tcg gcg ctc ggg ctg gag ccg ggg cgc gac gtg gac ctg 461
 Ala Asn Phe Ser Ala Leu Gly Leu Glu Pro Gly Arg Asp Val Asp Leu
 90 95 100 105

ggg cag ctg gag cag gag agc tgc ctg gat ggc tgg gag ttc agc cag 509
 Gly Gln Leu Glu Gln Glu Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln
 110 115 120

gac gtc tac ctg tcc acc gtc gtg acc gag tgg aat ctg gtg tgt gag 557
 Asp Val Tyr Leu Ser Thr Val Val Thr Glu Trp Asn Leu Val Cys Glu
 125 130 135

gac aac tgg aag gtg ccc ctc acc acc tcc ctg ttc ttc gta ggc gtg 605
 Asp Asn Trp Lys Val Pro Leu Thr Thr Ser Leu Phe Phe Val Gly Val
 140 145 150

ctc ctc ggc tcc ttc gtg tcc ggg cag ctg tca gac agg ttt ggc agg 653
 Leu Leu Gly Ser Phe Val Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg
 155 160 165

aag aac gtt ctc ttc gca acc atg gct gta cag act ggc ttc agc ttc 701
 Lys Asn Val Leu Phe Ala Thr Met Ala Val Gln Thr Gly Phe Ser Phe
 170 175 180 185

ctg cag att ttc tcc atc agc tgg gag atg ttc act gtg tta ttt gtc 749
 Leu Gln Ile Phe Ser Ile Ser Trp Glu Met Phe Thr Val Leu Phe Val
 190 195 200

atc gtg ggc atg ggc cag atc tcc aac tat gtg gta gcc ttc ata cta 797
 Ile Val Gly Met Gly Gln Ile Ser Asn Tyr Val Val Ala Phe Ile Leu
 205 210 215

gga aca gaa att ctt ggc aag tca gtt cgt att ata ttc tct aca tta 845

Gly Thr Glu Ile Leu Gly Lys Ser Val Arg Ile Ile Phe Ser Thr Leu
 220 225 230

gga gtg tgc aca ttt ttt gca gtt ggc tat atg ctg ctg cca ctg ttt 893
 Gly Val Cys Thr Phe Phe Ala Val Gly Tyr Met Leu Leu Pro Leu Phe
 235 240 245

gct tac ttc atc aga gac tgg cggtt atg ctg ctg gcgtt acgtt 941
 Ala Tyr Phe Ile Arg Asp Trp Arg Met Leu Leu Leu Ala Leu Thr Val
 250 255 260 265

ccg gga gtg ctg tgt gtc ccgtt ctg tgg ttc att cct gaa tct ccc 989
 Pro Gly Val Leu Cys Val Pro Leu Trp Trp Phe Ile Pro Glu Ser Pro
 270 275 280

cga tgg ctg ata tcc cag aga aga ttt aga gag gct gaa gat atc atc 1037
 Arg Trp Leu Ile Ser Gln Arg Arg Phe Arg Glu Ala Glu Asp Ile Ile
 285 290 295

caa aaa gct gca aaa atg aac aac aca gct gta cca gca gtg ata ttt 1085
 Gln Lys Ala Ala Lys Met Asn Asn Thr Ala Val Pro Ala Val Ile Phe
 300 305 310

gat tct gtg gag gag cta aat ccc ctg aag cag cag aaa gct ttc att 1133
 Asp Ser Val Glu Glu Leu Asn Pro Leu Lys Gln Gln Lys Ala Phe Ile
 315 320 325

ctg gac ctg ttc agg act cggtt aat att gcc ata atg acc att atg tct 1181
 Leu Asp Leu Phe Arg Thr Arg Asn Ile Ala Ile Met Thr Ile Met Ser
 330 335 340 345

ttg ctg cta tgg atg ctg acc tca gtg ggt tac ttt gct ctg tct ctg 1229
 Leu Leu Leu Trp Met Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu
 350 355 360

gat gct cct aat tta cat gga gat gcc tac ctg aac tgt ttc ctc tct 1277
 Asp Ala Pro Asn Leu His Gly Asp Ala Tyr Leu Asn Cys Phe Leu Ser
 365 370 375

gcc ttg att gaa att cca gct tac att aca gcc tgg ctg cta ttg cga 1325
 Ala Leu Ile Glu Ile Pro Ala Tyr Ile Thr Ala Trp Leu Leu Leu Arg
 380 385 390

acg ctg ccc agg cgt tat atc ata gct gca gta ctg ttc tgg gga gga 1373
 Thr Leu Pro Arg Arg Tyr Ile Ile Ala Ala Val Leu Phe Trp Gly Gly
 395 400 405

ggt gtg ctt ctc ttc att caa ctg gta cct gtg gat tat tac ttc tta 1421
 Gly Val Leu Leu Phe Ile Gln Leu Val Pro Val Asp Tyr Tyr Phe Leu
 410 415 420 425

tcc att ggt ctg gtc atg ctg gga aaa ttt ggg atc acc tct gct ttc 1469
 Ser Ile Gly Leu Val Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe
 430 435 440

tcc atg ctg tat gtc act gct gag ctc tac cca acc ctg gtc agg 1517
 Ser Met Leu Tyr Val Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg

A1

445	450	455	
aac atg gcg gtg ggg gtc aca tcc acg gcc tcc aga gtg ggc agc atc Asn Met Ala Val Gly Val Thr Ser Thr Ala Ser Arg Val Gly Ser Ile			1565
460	465	470	
att gcc ccc tac ttt gtt tac ctc ggt gct tac aac aga atg ctg ccc Ile Ala Pro Tyr Phe Val Tyr Leu Gly Ala Tyr Asn Arg Met Leu Pro			1613
475	480	485	
tac atc gtc atg ggt agt ctg act gtc ctg att gga atc ttc acc ctt Tyr Ile Val Met Gly Ser Leu Thr Val Leu Ile Gly Ile Phe Thr Leu			1661
490	495	500	505
A1 ttt ttc cct gaa agt ttg gga atg act ctt cca gaa acc tta gag cag Phe Phe Pro Glu Ser Leu Gly Met Thr Leu Pro Glu Thr Leu Glu Gln			1709
510	515	520	
atg cag aaa gtg aaa tgg ttc aga tct ggg aaa aaa aca aga gac tca Met Gln Lys Val Lys Trp Phe Arg Ser Gly Lys Lys Thr Arg Asp Ser			1757
525	530	535	
atg gag aca gaa gaa aat ccc aag gtt cta ata act gca ttc Met Glu Thr Glu Glu Asn Pro Lys Val Leu Ile Thr Ala Phe			1799
540	545	550	
tgaaaaaata tctaccccat ttggtaagt gaaaaacaga aaaataagac cctgtggaga			1859
aattcgttgt tcccactgaa atggactgac tgtaacgatt gacaccaaaa tgaaccttgc			1919
tatcaagaaa tgctcgcat acagtaaact ctggatgatt cttccagata atgtccttgc			1979
tttacaaacc aaccatttct agagagtctc cttactcatt aattcaatga aatggattgg			2039
taagatgtct tggaaacatg tttagtcaagg actggtaaaa tacatataaaa gattaacact			2099
catttccaat catacaaata ctatccaaat aaaaat			2135
<210> 3			
<211> 557			
<212> PRT			
<213> Homo sapiens			
<400> 3			
Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly			
1	5	10	15
Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro			
20	25	30	
Asn Gly Phe Thr Gly Leu Ser Ser Val Phe Leu Ile Ala Thr Pro Glu			
35	40	45	
His Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg			
50	55	60	
Asn His Thr Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His			

65

70

75

Ser Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu
 80 85 90 95

Gly Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu
 100 105 110

Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr
 115 120 125

Ile Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Ala Pro
 130 135 140

Leu Thr Ile Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Ile
 145 150 155

A1
 Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Val
 160 165 170 175

Thr Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Lys
 180 185 190

Asn Phe Glu Met Phe Val Val Leu Phe Val Leu Val Gly Met Gly Gln
 195 200 205

Ile Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Gly
 210 215 220

Lys Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Ile Phe Tyr
 225 230 235

Ala Phe Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp
 240 245 250 255

Trp Arg Met Leu Leu Val Ala Leu Thr Met Pro Gly Val Leu Cys Val
 260 265 270

Ala Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln
 275 280 285

Gly Arg Phe Glu Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ala
 290 295 300

Asn Gly Ile Val Val Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln
 305 310 315

Asp Leu Ser Ser Lys Lys Gln Gln Ser His Asn Ile Leu Asp Leu Leu
 320 325 330 335

Arg Thr Trp Asn Ile Arg Met Val Thr Ile Met Ser Ile Met Leu Trp
 340 345 350

Met Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn
 355 360 365

Leu His Gly Asp Ile Phe Val Asn Cys Phe Leu Ser Ala Met Val Glu

370

375

380

Val Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg
385 390 395

Arg Tyr Ser Met Ala Thr Ala Leu Phe Leu Gly Gly Ser Val Leu Leu
 400 405 410 415

Phe Met Gln Leu Val Pro Pro Asp Leu Tyr Tyr Leu Ala Thr Val Leu
420 425 430

Val Met Val Gly Lys Phe Gly Val Thr Ala Ala Phe Ser Met Val Tyr
 435 440 445

Val Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val
450 455 460

Gly Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr
465 470 475

Phe	Val	Tyr	Leu	Gly	Ala	Tyr	Asp	Arg	Phe	Leu	Pro	Tyr	Ile	Leu	Met
480					485					490					495

Gly Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Leu Pro Glu
500 505 510

Ser Phe Gly Thr Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val
 515 520 525

Lys Gly Met Lys His Arg Lys Thr Pro Ser His Thr Arg Met Leu Lys
 530 535 540

Asp Gly Gln Glu Arg Pro Thr Ile Leu Lys Ser Thr Ala Phe
545 550 555

<210> 4

<211> 1831

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (12)

<400> 4

cggacggtc

ggc atg cgg gac tac gac gag gtg acc gcc ttc ctg ggc gag tgg ggg

68

1 5 10 15

ccc ttc cag cgc ctc atc ttc ttc ctg ctc agc gcc agc atc atc atc ccc
Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro

216

aat ggc ttc acc ggc ctg tcc tcc gtg ttc ctg ata gcg acc ccg gag Asn Gly Phe Thr Gly Leu Ser Ser Val Phe Leu Ile Ala Thr Pro Glu 35 40 45	264
cac cgc tgc cggtg ccg gac gcc gcg aac ctg agc agc gcc tgg cgc His Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg 50 55 60	312
aac cac act gtc cca ctg cggtg gac ggc cgc gag gtg ccc cac Asn His Thr Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His 65 70 75	360
agc tgc cgc tac cggtg ctc gcc acc atc gcc aac ttc tgc gcg ctc Ser Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu 80 85 90 95	408
ggg ctg gag ccg ggg cgc gac gtg gac ctg ggg cag ctg gag cag gag Gly Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu 100 105 110	456
A1 agc tgt ctg gat ggc tgg gag ttc agt cag gac gtc tac ctg tcc acc Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr 115 120 125	504
att gtg acc gag tgg aac ctg gtg tgt gag gac gac tgg aag gcc cca Ile Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Ala Pro 130 135 140	552
ctc aca atc tcc ttg ttc gtg ggt gtg ctg ttg ggc tcc ttc att Leu Thr Ile Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Ile 145 150 155	600
tca ggg cag ctg tca gac agg ttt ggc cgg aag aat gtg ctg ttc gtg Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Val 160 165 170 175	648
acc atg ggc atg cag aca ggc ttc agc ttc ctg cag atc ttc tcg aag Thr Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Lys 180 185 190	696
aat ttt gag atg ttt gtc gtg ctg ttt gtc ctt gta ggc atg ggc cag Asn Phe Glu Met Phe Val Val Leu Phe Val Leu Val Gly Met Gly Gln 195 200 205	744
atc tcc aac tat gtg gca gca ttt gtc ctg ggg aca gaa att ctt ggc Ile Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Gly 210 215 220	792
aag tca gtt cgt ata ata ttc tct acg tta gga gtg tgc ata ttt tat Lys Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Ile Phe Tyr 225 230 235	840
gca ttt ggc tac atg gtg ctg cca ctg ttt gct tac ttc atc cga gac Ala Phe Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp 240 245 250 255	888
tgg cggtg atg ctg ctg gtg gcg ctg acg atg ccg ggg gtg ctg tgc gtg	936

Trp Arg Met Leu Leu Val Ala Leu Thr Met Pro Gly Val Leu Cys Val			
260	265	270	
gca ctc tgg tgg ttc atc cct gag tcc ccc cga tgg ctc atc tct cag			984
Ala Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln			
275	280	285	
gga cga ttt gaa gag gca gag gtg atc atc cgc aag gct gcc aaa gcc			1032
Gly Arg Phe Glu Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ala			
290	295	300	
aat ggg att gtt gtg cct tcc act atc ttt gac ccg agt gag tta caa			1080
Asn Gly Ile Val Val Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln			
305	310	315	
gac cta agt tcc aag aag cag cag tcc cac aac att ctg gat ctg ctt			1128
Asp Leu Ser Ser Lys Lys Gln Gln Ser His Asn Ile Leu Asp Leu Leu			
320	325	330	335
A1			
cga acc tgg aat atc cgg atg gtc acc atc atg tcc ata atg ctg tgg			1176
Arg Thr Trp Asn Ile Arg Met Val Thr Ile Met Ser Ile Met Leu Trp			
340	345	350	
atg acc ata tca gtg ggc tat ttt ggg ctt tcg ctt gat act cct aac			1224
Met Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn			
355	360	365	
ttg cat ggg gac atc ttt gtg aac tgc ttc ctt tca gcg atg gtt gaa			1272
Leu His Gly Asp Ile Phe Val Asn Cys Phe Leu Ser Ala Met Val Glu			
370	375	380	
gtc cca gca tat gtg ttg gcc tgg ctg ctg ctg caa tat ttg ccc cgg			1320
Val Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg			
385	390	395	
cgc tat tcc atg gcc act gcc ctc ttc ctg ggt ggc agt gtc ctt ctc			1368
Arg Tyr Ser Met Ala Thr Ala Leu Phe Leu Gly Gly Ser Val Leu Leu			
400	405	410	415
ttc atg cag ctg gta ccc cca gac ttg tat tat ttg gct aca gtc ctg			1416
Phe Met Gln Leu Val Pro Pro Asp Leu Tyr Tyr Leu Ala Thr Val Leu			
420	425	430	
gtg atg gtg ggc aag ttt gga gtc acg gct gcc ttt tcc atg gtc tac			1464
Val Met Val Gly Lys Phe Gly Val Thr Ala Ala Phe Ser Met Val Tyr			
435	440	445	
gtg tac aca gcc gag ctg tat ccc aca gtg gtg aga aac atg ggt gtg			1512
Val Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val			
450	455	460	
gga gtc agc tcc aca gca tcc cgc ctg ggc agc atc ctg tct ccc tac			1560
Gly Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr			
465	470	475	
ttc gtt tac ctt ggt gcc tac gac cgc ttc ctg ccc tac att ctc atg			1608
Phe Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met			

480	485	490	495	
gga agt ctg acc atc ctg aca gcc atc ctc acc ttg ttt ctc cca gag Gly Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Leu Pro Glu				1656
	500	505		510
agc ttc ggt acc cca ctc cca gac acc att gac cag atg cta aga gtc Ser Phe Gly Thr Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val				1704
	515	520		525
aaa gga atg aaa cac aga aaa act cca agt cac aca agg atg tta aaa Lys Gly Met Lys His Arg Lys Thr Pro Ser His Thr Arg Met Leu Lys				1752
	530	535		540
gat ggt caa gaa agg ccc aca atc ctt aaa agc aca gcc ttc Asp Gly Gln Glu Arg Pro Thr Ile Leu Lys Ser Thr Ala Phe				1794
	545	550		555
taacatcgact tccagaataqq qagaactqa aqaggaa				1831

A1

```
<210> 5
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer
Sequence

<400> 5
ctataacgac tcactatagg gc 22

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer
Sequence

<400> 6
tgtagcgtga agacgcacaga a 21

<210> 7
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer
Sequence

<400> 7
tcgagcggcc gcccgggcag gt 22

<210> 8
```

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 8
aggcggtggt gcggaggggcg gt 22

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

A1 <400> 9
cttttgagca agttcagcct 20
<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 10
agaggtggct tatgagtatt tctt 24
<210> 11
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 11
ccagggtttt cccagtcacg ac 22

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 12

tcacacagga aacagctatg ac	22
<210> 13	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence	
<400> 13	
gtgctgttgg gctccttcat ttca	24
<210> 14	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence	
A1	
<400> 14	
agctgcata agagaaggac actg	24
<210> 15	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence	
<400> 15	
agcatccctgt ctccctactt cgtt	24
<210> 16	
<211> 33	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence	
<400> 16	
gatggatccc ggacggtctt gggtcgcctg ctg	33
<210> 17	
<211> 33	
<212> DNA	
<213> Artificial Sequence	

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 17
gatggatcca aatgctgcc a catagttgga gat 33

<210> 18
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 18
gatggatcca tgggcatgca gacaggcttc agc 33

<210> 19
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 19
gatggatcct tcctcttcag ttttccctt act 33

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 20
cgccgcgaat cgctgaatcc ttcc 24

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 21
aggctttga tttgttgt tgag 24

<210> 22
<211> 553

A1

<212> PRT

<213> Mus musculus

<400> 22

Met	Arg	Asp	Tyr	Asp	Glu	Val	Ile	Ala	Phe	Leu	Gly	Glu	Trp	Gly	Pro
1															15

Phe	Gln	Arg	Leu	Ile	Phe	Phe	Leu	Leu	Ser	Ala	Ser	Ile	Ile	Pro	Asn
															30
20							25								

Gly	Phe	Asn	Gly	Met	Ser	Val	Val	Phe	Leu	Ala	Gly	Thr	Pro	Glu	His
															45
35							40								

Arg	Cys	Leu	Val	Pro	Asp	Thr	Val	Asn	Leu	Ser	Ser	Ser	Trp	Arg	Asn
															50
							55								60

His	Ser	Ile	Pro	Leu	Glu	Thr	Lys	Asp	Gly	Arg	Gln	Val	Pro	Gln	Ser
															80
65							70				75				

Cys	Arg	Arg	Tyr	Arg	Leu	Ala	Thr	Ile	Ala	Asn	Phe	Ser	Ala	Met	Gly
															95
							85				90				

Leu	Glu	Pro	Gly	Gln	Asp	Val	Asp	Leu	Glu	Gln	Leu	Glu	Gln	Glu	Ser
															110
100							105								

Cys	Leu	Asp	Gly	Trp	Glu	Tyr	Asp	Lys	Asp	Ile	Phe	Leu	Ser	Thr	Ile
															115
							120								125

Val	Thr	Glu	Trp	Asn	Leu	Val	Cys	Glu	Asp	Asp	Trp	Lys	Thr	Pro	Leu
															130
							135					140			

Thr	Thr	Ser	Leu	Phe	Phe	Val	Gly	Val	Leu	Cys	Gly	Ser	Phe	Val	Ser
															145
							150				155				160

Gly	Gln	Leu	Ser	Asp	Arg	Phe	Gly	Arg	Lys	Lys	Val	Leu	Phe	Ala	Thr
															165
							165				170				175

Met	Ala	Val	Gln	Thr	Gly	Phe	Ser	Phe	Val	Gln	Ile	Phe	Ser	Thr	Asn
															180
							180				185				190

Trp	Glu	Met	Phe	Thr	Val	Leu	Phe	Ala	Ile	Val	Gly	Met	Gly	Gln	Ile
															195
							200					205			

Ser	Asn	Tyr	Val	Val	Ala	Phe	Ile	Leu	Gly	Thr	Glu	Ile	Leu	Ser	Lys
															210
							215				220				

Ser	Val	Arg	Ile	Ile	Phe	Ser	Thr	Leu	Gly	Val	Cys	Thr	Phe	Phe	Ala
															225
							230				235				240

Ile	Gly	Tyr	Met	Val	Leu	Pro	Leu	Phe	Ala	Tyr	Phe	Ile	Arg	Asp	Trp
															245
							245				250				255

Arg	Met	Leu	Leu	Leu	Ala	Leu	Thr	Leu	Pro	Gly	Leu	Phe	Cys	Val	Pro
															260
							260				265				270

Leu	Trp	Trp	Phe	Ile	Pro	Glu	Ser	Pro	Arg	Trp	Leu	Ile	Ser	Gln	Arg
															275
							275				280				285

A1

Arg Phe Ala Glu Ala Glu Gln Ile Ile Gln Lys Ala Ala Lys Met Asn
 290 295 300
 Ser Ile Val Ala Pro Ala Gly Ile Phe Asp Pro Leu Glu Leu Gln Glu
 305 310 315 320
 Leu Asn Ser Leu Lys Gln Gln Lys Val Ile Ile Leu Asp Leu Phe Arg
 325 330 335
 Thr Arg Asn Ile Ala Thr Ile Thr Val Met Ala Val Met Leu Trp Met
 340 345 350
 Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu Asn Val Pro Asn Leu
 355 360 365
 His Gly Asp Val Tyr Leu Asn Cys Phe Leu Ser Gly Leu Ile Glu Val
 370 375 380
A1
 Pro Ala Tyr Phe Thr Ala Trp Leu Leu Leu Arg Thr Leu Pro Arg Arg
 385 390 395 400
 Tyr Ile Ile Ala Gly Val Leu Phe Trp Gly Gly Gly Val Leu Leu Leu
 405 410 415
 Ile Gln Val Val Pro Glu Asp Tyr Asn Phe Val Ser Ile Gly Leu Val
 420 425 430
 Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val
 435 440 445
 Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly
 450 455 460
 Ile Thr Ser Met Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe
 465 470 475 480
 Val Tyr Leu Gly Ala Tyr Asn Arg Leu Leu Pro Tyr Ile Leu Met Gly
 485 490 495
 Ser Leu Thr Val Leu Ile Gly Ile Ile Thr Leu Phe Phe Pro Glu Ser
 500 505 510
 Phe Gly Val Thr Leu Pro Glu Asn Leu Glu Gln Met Gln Lys Val Arg
 515 520 525
 Gly Phe Arg Cys Gly Lys Lys Ser Thr Val Ser Val Asp Arg Glu Glu
 530 535 540
 Ser Pro Lys Val Leu Ile Thr Ala Phe
 545 550
 <210> 23
 <211> 2083
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (122)..(1780)

<400> 23 attcggcaca ggacggcggtg tttgacgagc cacctaggaa gatccctca gcgcgccaa tcgctgaatc ctttctctcc acccacctcc ctcacgcaag ctgaggagga gaggtggaaa c atg cg ^g gac tac gac gag gtg atc gcc ttc ctg ggc gag tgg ggg ccc Met Arg Asp Tyr Asp Glu Val Ile Ala Phe Leu Gly Glu Trp Gly Pro 1 5 10 15 ttc cag cgc ctc atc ttc ttt ctg ctc agc gcc agc atc atc ccc aat Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn 20 25 30 ggc ttc aat ggt atg tca gtc gtg ttc ctg gcg ggg acc ccc gag cac Gly Phe Asn Gly Met Ser Val Val Phe Leu Ala Gly Thr Pro Glu His 35 40 45 cgt tgc ctg gtt cct gac act gtg aac ctg agc agc tcc tgg cgc aac Arg Cys Leu Val Pro Asp Thr Val Asn Leu Ser Ser Ser Trp Arg Asn 50 55 60 cac agc atc ccc ttg gag acg aag gac gga cga cag gtg cct cag agc His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Ser 65 70 75 80 tgc cgc cgc tac cga ctg gcc acc atc gcc aac ttc tct gcg atg ggg Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Met Gly 85 90 95 ctg gag cca gga cag gac gtg gat ctg gag cag ctg gag cag gag agc Leu Glu Pro Gly Gln Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser 100 105 110 tgc ctg gat ggc tgg gag tac gac aag gac atc ttc ctg tcc acc atc Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Ile Phe Leu Ser Thr Ile 115 120 125 gtg aca gag tgg aat ctg gtg tgt gag gat gac tgg aag aca ccc ctc Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Thr Pro Leu 130 135 140 acc acc tcc ctg ttc gta ggc gtt ctc tgc ggc tcc ttc gtg tct Thr Thr Ser Leu Phe Phe Val Gly Val Leu Cys Gly Ser Phe Val Ser 145 150 155 160 ggg cag ctg tca gac agg ttt ggc agg aag aaa gtc ctc ttt gca acc Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Lys Val Leu Phe Ala Thr 165 170 175 atg gct gtg cag act gga ttc agc ttc gtg cag att ttc tca acc aac Met Ala Val Gln Thr Gly Phe Ser Phe Val Gln Ile Phe Ser Thr Asn 180 185 190 tgg gag atg ttc act gtg ttg ttt gcc att gtg ggc atg ggc cag atc	60 120 169 217 265 313 361 409 457 505 553 601 649 697 745
---	--

A1

Trp Glu Met Phe Thr Val Leu Phe Ala Ile Val Gly Met Gly Gln Ile				
195	200	205		
tcc aac tac gtg gtg gcc ttc ata cta gga act gaa atc ctg agc aag				793
Ser Asn Tyr Val Val Ala Phe Ile Leu Gly Thr Glu Ile Leu Ser Lys				
210	215	220		
tcg gtt cgc atc atc ttc tcc aca tta gga gtc tgt aca ttt ttt gca				841
Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala				
225	230	235	240	
atc ggc tac atg gtc ctg ccg ctg ttt gca tac ttc atc aga gac tgg				889
Ile Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp				
245	250	255		
agg atg ctg ctg ctg gcc ctg aca ctg cct ggc ctg ttc tgt gtt ccc				937
Arg Met Leu Leu Leu Ala Leu Thr Leu Pro Gly Leu Phe Cys Val Pro				
260	265	270		
ctg tgg tgg ttt att cca gaa tct ccc cgg tgg ctg ata tcc cag agg				985
Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg				
275	280	285		
<i>A1</i>				
aga ttt gca gag gcc gaa cag atc atc cag aaa gcc gca aag atg aac				1033
Arg Phe Ala Glu Ala Glu Gln Ile Ile Gln Lys Ala Ala Lys Met Asn				
290	295	300		
agc atc gtg gcg cca gca ggg ata ttc gat cct cta gag cta cag gag				1081
Ser Ile Val Ala Pro Ala Gly Ile Phe Asp Pro Leu Glu Leu Gln Glu				
305	310	315	320	
cta aac tcc ttg aag cag cag aaa gtc ata atc ctg gac ctg ttc agg				1129
Leu Asn Ser Leu Lys Gln Gln Lys Val Ile Ile Leu Asp Leu Phe Arg				
325	330	335		
act cggtt aac att gcc acc ata acc gtg atg gct gtg atg ctg tgg atg				1177
Thr Arg Asn Ile Ala Thr Ile Thr Val Met Ala Val Met Leu Trp Met				
340	345	350		
cta acc tca gtg ggt tac ttt gct ctg tct ctc aat gtt cct aat tta				1225
Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu Asn Val Pro Asn Leu				
355	360	365		
cat gga gat gtc tac ctg aac tgc ttc ctc tct ggc ctg att gaa gtt				1273
His Gly Asp Val Tyr Leu Asn Cys Phe Leu Ser Gly Leu Ile Glu Val				
370	375	380		
cca gct tac ttc aca gcc tgg ctg cta ctg cga acc ctg cca cgg aga				1321
Pro Ala Tyr Phe Thr Ala Trp Leu Leu Leu Arg Thr Leu Pro Arg Arg				
385	390	395	400	
tat att ata gct ggg gtg cta ttc tgg gga gga ggt gtg ctt ctc ttg				1369
Tyr Ile Ile Ala Gly Val Leu Phe Trp Gly Gly Val Leu Leu Leu				
405	410	415		
atc caa gtg gta cct gaa gat tat aac ttt gtg tcc att gga ctg gtg				1417
Ile Gln Val Val Pro Glu Asp Tyr Asn Phe Val Ser Ile Gly Leu Val				

420

425

430

atg ctg ggg aaa ttt ggg atc acc tct gcc ttc tcc atg ttg tat gtc 1465
 Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val
 435 440 445

ttc act gcg gag ctc tac cca acc ctg gtc agg aac atg gct gtg ggc 1513
 Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly
 450 455 460

atc acc tcc atg gcc tct cggtt ggc agc atc att gcc ccc tat ttc 1561
 Ile Thr Ser Met Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe
 465 470 475 480

gtt tac ctg ggc gcc tat aac aga ctc cta ccc tac atc ctc atg ggc 1609
 Val Tyr Leu Gly Ala Tyr Asn Arg Leu Leu Pro Tyr Ile Leu Met Gly
 485 490 495

agt ctg act gtc ctc att gga atc atc acg ctt ttt ttc cct gaa agt 1657
 Ser Leu Thr Val Leu Ile Gly Ile Ile Thr Leu Phe Phe Pro Glu Ser
 500 505 510

A1 ttt gga gtg act cta cca gag aac ttg gag cag atg cag aaa gtg aga 1705
 Phe Gly Val Thr Leu Pro Glu Asn Leu Glu Gln Met Gln Lys Val Arg
 515 520 525

ggg ttc aga tgt ggg aaa aaa tca aca gtc tca gtg gac aga gaa gaa 1753
 Gly Phe Arg Cys Gly Lys Ser Thr Val Ser Val Asp Arg Glu Glu
 530 535 540

agc ccc aag gtt cta ata act gca ttc taacgagggtt tccaaggcac 1800
 Ser Pro Lys Val Leu Ile Thr Ala Phe
 545 550

ttggcaaact gaaaagcaga tgtatacat gagcagggtg tgatagagca agcctgcaat 1860

cccagcgctc ttgggtgga gacagaagat caggagttca aggtcatcct tggctacagc 1920

aggagtgtaa gaccagcctg tcttaccaca agcaaccctg tctcaacaga acaaatcaaa 1980

agcctttct gctgaaaggg attaacagaa acaatgagca ccaaactgga cttgtggaga 2040

aatgcacact atctcatgaa ttctggccca ctcttccaga tgg 2083

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 24

cccatccaa caaggacaaa aagc

24

<210> 25

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 25
 acagaacaga aaagccctca gtca 24

<210> 26
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 26
 tggtttcgt gggtgtgctg atgg 24

A1

<210> 27
 <211> 557
 <212> PRT
 <213> Mus musculus

<400> 27
 Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly Pro
 1 5 10 15

Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
 20 25 30

Gly Phe Asn Gly Met Ser Ile Val Phe Leu Ala Gly Thr Pro Glu His
 35 40 45

Arg Cys Leu Val Pro His Thr Val Asn Leu Ser Ser Ala Trp Arg Asn
 50 55 60

His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Lys
 65 70 75 80

Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Glu Leu Gly
 85 90 95

Leu Glu Pro Gly Arg Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
 100 105 110

Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Val Phe Leu Ser Thr Ile
 115 120 125

Val Thr Glu Trp Asp Leu Val Cys Lys Asp Asp Trp Lys Ala Pro Leu
 130 135 140

Thr Thr Ser Leu Phe Phe Val Gly Val Leu Met Gly Ser Phe Ile Ser

145	150	155	160
Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Leu Thr			
165	170	175	
Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Val Phe Ser Val Asn			
180	185	190	
Phe Glu Met Phe Thr Val Leu Phe Val Leu Val Gly Met Gly Gln Ile			
195	200	205	
Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Ser Lys			
210	215	220	
Ser Ile Arg Ile Ile Phe Ala Thr Leu Gly Val Cys Ile Phe Tyr Ala			
225	230	235	240
Phe Gly Phe Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp			
245	250	255	
Arg Met Leu Leu Leu Ala Leu Thr Val Pro Gly Val Leu Cys Gly Ala			
260	265	270	
AJ			
Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Gly			
275	280	285	
Arg Ile Lys Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ile Asn			
290	295	300	
Gly Ile Val Ala Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln Asp			
305	310	315	320
Leu Asn Ser Thr Lys Pro Gln Leu His His Ile Tyr Asp Leu Ile Arg			
325	330	335	
Thr Arg Asn Ile Arg Val Ile Thr Ile Met Ser Ile Ile Leu Trp Leu			
340	345	350	
Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn Leu			
355	360	365	
His Gly Asp Ile Tyr Val Asn Cys Phe Leu Leu Ala Ala Val Glu Val			
370	375	380	
Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg Arg			
385	390	395	400
Tyr Ser Ile Ser Ala Ala Leu Phe Leu Gly Gly Ser Val Leu Leu Phe			
405	410	415	
Met Gln Leu Val Pro Ser Glu Leu Phe Tyr Leu Ser Thr Ala Leu Val			
420	425	430	
Met Val Gly Lys Phe Gly Ile Thr Ser Ala Tyr Ser Met Val Tyr Val			
435	440	445	
Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val Gly			

450	455	460	
Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr Phe			
465	470	475	480
Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met Gly			
485	490	495	
Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Phe Pro Glu Ser			
500	505	510	
Phe Gly Val Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val Lys			
515	520	525	
Gly Ile Lys Gln Trp Gln Ile Gln Ser Gln Thr Arg Met Gln Lys Asp			
530	535	540	
Gly Glu Glu Ser Pro Thr Val Leu Lys Ser Thr Ala Phe			
545	550	555	
 <i>A1</i>			
<210> 28			
<211> 1888			
<212> DNA			
<213> Mus musculus			
<220>			
<221> CDS			
<222> (60)..(1730)			
<400> 28			
ctcccgcgcc acggtgtccc cttattccca tacgggcgct gtgggaggct gaggacggc			59
atg cgg gac tac gac gag gtg acc gcc ttc cta ggc gag tgg ggg ccc			107
Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly Pro			
1	5	10	15
ttc cag cgc ctc atc ttc ctg ctc agc gcc agc atc atc ccc aat			155
Phe Gln Arg Leu Ile Phe Leu Ser Ala Ser Ile Ile Pro Asn			
20	25	30	
ggc ttc aat ggt atg tcc atc gtg ttc ctg gcg ggg acc ccg gag cac			203
Gly Phe Asn Gly Met Ser Ile Val Phe Leu Ala Gly Thr Pro Glu His			
35	40	45	
cgt tgc ctt gtg cct cac acc gtg aac ctg agc agc gcg tgg cgc aac			251
Arg Cys Leu Val Pro His Thr Val Asn Leu Ser Ser Ala Trp Arg Asn			
50	55	60	
cac agt atc ccg ttg gag acg aag gac gga cga cag gtg cct cag aaa			299
His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Lys			
65	70	75	80
tgc cgc cgc tac cga ctg gcc acc atc gcc aac ttc tct gag cta ggg			347
Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Glu Leu Gly			
85	90	95	
ctg gag ccg ggg cg gac gtg gac ctg gag cag ctg gag cag gag agc			395

Leu Glu Pro Gly Arg Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
 100 105 110

tgc ctg gat ggc tgg gag tac gac aag gac gtc ttc ctg tcc acc atc 443
 Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Val Phe Leu Ser Thr Ile
 115 120 125

gtg aca gag tgg gac ctg gtg tgt aag gat gac tgg aaa gcc cca ctc 491
 Val Thr Glu Trp Asp Leu Val Cys Lys Asp Asp Trp Lys Ala Pro Leu
 130 135 140

acc acc tcc ttg ttt ttc gtg ggt gtg ctg atg ggc tcc ttc att tca 539
 Thr Thr Ser Leu Phe Phe Val Gly Val Leu Met Gly Ser Phe Ile Ser
 145 150 155 160

gga cag ctc tca gac agg ttt ggt cgc aag aat gtg ctg ttt ttg acc 587
 Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Leu Thr
 165 170 175

A1 atg ggc atg cag act ggc ttc agc ttc ctg cag gtc ttc tct gtg aac 635
 Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Val Phe Ser Val Asn
 180 185 190

ttc gag atg ttt aca gtg ctt ttt gtc ctt gtt ggc atg ggt cag atc 683
 Phe Glu Met Phe Thr Val Leu Phe Val Leu Val Gly Met Gly Gln Ile
 195 200 205

tcc aac tac gtg gca gca ttt gtc ctg gga aca gaa att ctt tcc aag 731
 Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Ser Lys
 210 215 220

tca att cga att ata ttc gcc acc tta gga gtt tgc ata ttt tat gcg 779
 Ser Ile Arg Ile Ile Phe Ala Thr Leu Gly Val Cys Ile Phe Tyr Ala
 225 230 235 240

ttt ggc ttc atg gtg ctg cca ctg ttt gca tac ttc atc aga gac tgg 827
 Phe Gly Phe Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
 245 250 255

agg atg ctg ctg gcg ctc act gtg cca ggg gtg cta tgt ggg gct 875
 Arg Met Leu Leu Ala Leu Thr Val Pro Gly Val Leu Cys Gly Ala
 260 265 270

ctc tgg tgg ttc atc cct gag tcc cca cga tgg ctc atc tct caa ggc 923
 Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Gly
 275 280 285

cga att aaa gag gca gag gtg atc atc cgc aaa gct gcc aaa atc aat 971
 Arg Ile Lys Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ile Asn
 290 295 300

ggg att gtt gca cct tcc act atc ttc gat cca agt gag tta caa gac 1019
 Gly Ile Val Ala Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln Asp
 305 310 315 320

tta aat tct acg aag cct cag ttg cac cac att tat gat ctg atc cga 1067
 Leu Asn Ser Thr Lys Pro Gln Leu His His Ile Tyr Asp Leu Ile Arg

325	330	335	
aca cg aat atc agg gtc atc acc atc atg tct ata atc ctg tgg ctg Thr Arg Asn Ile Arg Val Ile Thr Ile Met Ser Ile Ile Leu Trp Leu			1115
340	345	350	
acc ata tca gtg ggc tat ttt gga cta tct ctt gac act cct aac ttg Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn Leu			1163
355	360	365	
cat ggg gac atc tat gtg aac tgc ttc cta ctg gcg gct gtt gaa gtc His Gly Asp Ile Tyr Val Asn Cys Phe Leu Leu Ala Ala Val Glu Val			1211
370	375	380	
cca gcc tat gtg ctg gcc tgg ctg ttg cag tac ttg ccc cgg cga Pro Ala Tyr Val Leu Ala Trp Leu Leu Gln Tyr Leu Pro Arg Arg			1259
385	390	395	400
tat tct atc tcg gct gcc ctt ttc ctg ggt ggc agt gtc ctt ctc ttc Tyr Ser Ile Ser Ala Ala Leu Phe Leu Gly Gly Ser Val Leu Leu Phe			1307
405	410	415	
<i>A1</i>			
atg cag ctg gtg cct tca gaa ttg ttt tac ttg tcc act gcc ctg gtg Met Gln Leu Val Pro Ser Glu Leu Phe Tyr Leu Ser Thr Ala Leu Val			1355
420	425	430	
atg gtg ggg aag ttt gga atc acc tct gcc tac tcc atg gtc tat gtg Met Val Gly Lys Phe Gly Ile Thr Ser Ala Tyr Ser Met Val Tyr Val			1403
435	440	445	
tac aca gct gag ctg tac ccc act gtg gtc aga aac atg ggt gtg ggg Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val Gly			1451
450	455	460	
gtc agc tcc aca gca tcc cgc ctt ggc agc atc ctg tct ccc tac ttt Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr Phe			1499
465	470	475	480
gtt tac cta ggt gcc tat gat cgc ttc ctg cct tat att ctc atg gga Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met Gly			1547
485	490	495	
agt ctg acc atc ctg aca gct atc ctc acc ttg ttc ttc cct gag agc Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Phe Pro Glu Ser			1595
500	505	510	
ttt ggt gtc cct ctc cca gat acc att gac cag atg cta agg gtc aaa Phe Gly Val Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val Lys			1643
515	520	525	
gga ata aaa cag tgg caa atc caa agc cag aca aga atg caa aaa gat Gly Ile Lys Gln Trp Gln Ile Gln Ser Gln Thr Arg Met Gln Lys Asp			1691
530	535	540	
ggt gaa gaa agc cca aca gtc cta aag agc aca gcc ttc taacaccctg Gly Glu Glu Ser Pro Thr Val Leu Lys Ser Thr Ala Phe			1740
545	550	555	

tccagaaggc aaaaaactga ttggaaacct tcataatgtc agaaatgctc tccatgactg 1800
 agggctttc tggtctgtta accttgcgtc taacatgctc atggattggg gcatctgtcc 1860
 tggagagtca ctttcctcta gggacacc 1888

 <210> 29
 <211> 44
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

 <400> 29
 ctaatacgac tcactatagg gctcgagcgg ccgcggggc aggt 44

 <210> 30
 <211> 43
 <212> DNA
 <213> Artificial Sequence

A1
 <220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequencence

 <400> 30
 tgttagcgtga agacgacaga aagggcgtgg tgcggaggc ggt 43

 <210> 31
 <211> 10
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

 <400> 31
 acctgccccgg 10

 <210> 32
 <211> 11
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

 <400> 32
 accggccctcc g 11